FIG. 1

```
1     GAGGTCCAGC TTCAGCAGTC TGGACCTGAC CTGGTGAAGC CTGGGGCTTC
        E  V  Q   L  Q  Q  S   G  P  D   L  V  K   P  G  A  S

51    AGTGAAGATA TCCTGCAAGG CTTCTGGTTA CTCATTCACT GGCTACTACA
        V  K  I   S  C  K   A  S  G  Y   S  F  T   G  Y  Y

101   TGCACTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGACGT
      M  H  W  V   K  Q  S   H  G  K   S  L  E  W   I  G  R

151   ATTAATCCTA ACAATGGTGT TACTCTCTAC AACCAGAAAT TCAAGGACAA
        I  N  P   N  N  G  V   T  L  Y   N  Q  K   F  K  D  K

201   GGCCATATTA ACTGTAGACA AGTCATCCAC CACAGCCTAC ATGGAGCTCC
        A  I  L   T  V  D   K  S  S  T   T  A  Y   M  E  L

251   GCAGCCTGAC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGATCTACT
      R  S  L  T   S  E  D   S  A  V   Y  Y  C  A   R  S  T

301   ATGATTACGA ACTATGTTAT GGACTACTGG GGTCAAGTAA CCTCAGTCAC
      M  I  T   N  Y  V  M   D  Y  W   G  Q  V   T  S  V  T

351   CGTCTCCTCA GGTGGTGGTG GGAGCGGTGG TGGCGGCACT GGCGGCGGCG
        V  S  S   G  G  G   G  S  G  G   G  G  T   G  G  G

401   GATCTAGTAT TGTGATGACC CAGACTCCCA CATTCCTGCT TGTTTCAGCA
      G  S  S  I   V  M  T   Q  T  P   T  F  L  L   V  S  A

451   GGAGACAGGG TTACCATAAC CTGCAAGGCC AGTCAGAGTG TGAGTAATGA
        C  D  R   V  T  I  T   C  K  A   S  Q  S   V  S  N  D

501   TGTAGDTTGG TACCAACAGA AGCCAGGGCA GTCTCCTACA CTGCTCATAT
        V  A  W   Y  Q  Q   K  P  C  Q   S  P  T   L  L  I

551   CCTATACATC CAGTCGCTAC GCTGGAGTCC CTGATCGCTT CATTGGCAGT
      S  Y  T  S   S  R  Y   A  G  V   P  D  R  F   I  G  S

601   GGATATGGGA CGGATTTCAC TTTCACCATC AGCACTTTGC AGGCTGAAGA
        G  Y  G   T  D  F  T   F  T  I   S  T  L   Q  A  E  D

651   CCTGGCAGTT TATTTCTGTC AGCAAGATTA TAATTCTCCT CCGACGTTCG
        L  A  V   Y  F  C   Q  Q  D  Y   N  S  P   P  T  F

701   GTGGAGGCAC CAAGCTGGAA ATCAAACGG
      G  G  G  T   K  L  E   I  K  R
```

FIG. 2

```
ATGGGCCACA CACGGAGGCA GGGAACATCA CCATCCAAGT GTCCATACCT    50
 M  G  H   T  R  R  Q   G  T  S   P  S  K   C  P  Y  L

CAATTTCTTT CAGCTCTTGG TGCTGGCTGG TCTTTCTCAC TTCTGTTCAG   100
 N  F  F   Q  L  L   V  L  A  G   L  S  H   F  C  S

GTGTTATCCA CGTGACCAAG GAAGTGAAAG AAGTGGCAAC GCTGTCCTGT   150
G  V  I  H   V  T  K   E  V  K   E  V  A  T   L  S  C

GGTCACAATG TTTCTGTTGA AGAGCTGGCA CAAACTCGCA TCTACTGGCA   200
 G  H  N   V  S  V  E   E  L  A   Q  T  R   I  Y  W  Q

AAAGGAGAAG AAAATGGTGC TGACTATGAT GTCTGGGGAC ATGAATATAT   250
 K  E  K   K  M  V   L  T  M  M   S  G  D   M  N  I

GGCCCGAGTA CAAGAACCGG ACCATCTTTG ATATCACTAA TAACCTCTCC   300
W  P  E  Y   K  N  R   T  I  F   D  I  T  N   N  L  S

ATTGTGATCC TGGCTCTGCG CCCATCTGAC GAGGGCACAT ACGAGTGTGT   350
 I  V  I   L  A  L  R   P  S  D   E  G  T   Y  E  C  V

TGTTCTGAAG TATGAAAAAG ACGCTTTCAA GCGGGAACAC CTGGCTGAAG   400
 V  L  K   Y  E  K   D  A  F  K   R  E  H   L  A  E

TGACGTTATC AGTCAAAGCT GACTTCCCTA CACCTAGTAT ATCTGACTTT   450
V  T  L  S   V  K  A   D  F  P   T  P  S  I   S  D  F

GAAATTCCAA CTTCTAATAT TAGAAGGATA ATTTGCTCAA CCTCTGGAGG   500
 E  I  P   T  S  N  I   R  R  I   I  C  S   T  S  G  G

TTTTCCAGAG CCTCACCTCT CCTGGTTGGA AAATGGAGAA GAATTAAATG   550
 F  P  E   P  H  L   S  W  L  E   N  G  E   E  L  N

CCATCAACAC AACAGTTTCC CAAGATCCTG AAACTGAGCT CTATGCTGTT   600
A  I  N  T   T  V  S   Q  D  P   E  T  E  L   Y  A  V

AGCAGCAAAC TGGATTTCAA TATGACAACC AACCACAGCT TCATGTGTCT   650
 S  S  K   L  D  F  N   M  T  T   N  H  S   F  M  C  L

CATCAAGTAT GGACATTTAA GAGTGAATCA GACCTTCAAC TGGAATACAA   700
 I  K  Y   G  H  L   R  V  N  Q   T  F  N   W  N  T

CCAAGCAAGA GCATTTTCCT GATGGAGGCG GGGGATCCGA GGTCCAGCTT   750
T  K  Q  E   H  F  P   D  G  G   G  G  S  E   V  Q  L
```

```
CAGCAGTCTG GACCTGACCT GGTGAAGCCT GGGGCTTCAG TGAAGATATC    800
 Q  Q  S   G  P  D  L   V  K  P   G  A  S   V  K  I  S

CTGCAAGGCT TCTGGTTACT CATTCACTGG CTACTACATG CACTGGGTGA    850
  C  K  A   S  G  Y   S  F  T  G   Y  Y  M   H  W  V

AGCAGAGCCA TGGAAAGAGC CTTGAGTGGA TTGGACGTAT TAATCCTAAC    900
K  Q  S  H   G  K  S   L  E  W   I  G  R  I   N  P  N

AATGGTGTTA CTCTCTACAA CCAGAAATTC AAGGACAAGG CCATATTAAC    950
 N  G  V   T  L  Y  N   Q  K  F   K  D  K   A  I  L  T

TGTAGACAAG TCATCCACCA CAGCCTACAT GGAGCTCCGC AGCCTGACAT    1000
  V  D  K   S  S  T   T  A  Y  M   E  L  R   S  L  T

CTGAGGACTC TGCGGTCTAT TACTGTGCAA GATCTACTAT GATTACGAAC    1050
S  E  D  S   A  V  Y   Y  C  A   R  S  T  M   I  T  N

TATGTTATGG ACTACTGGGG TCAAGTAACC TCAGTCACCG TCTCCTCAGG    1100
 Y  V  M   D  Y  W  G   Q  V  T   S  V  T   V  S  S  G

TGGTGGTGGG AGCGGTGGTG GCGGCACTGG CGGCGGCGGA TCTAGTATTG    1150
  G  G  G   S  G  G   G  G  T  G   G  G  G   S  S  I

TGATGACCCA GACTCCCACA TTCCTGCTTG TTTCAGCAGG AGACACCGTT    1200
V  M  T  Q   T  P  T   F  L  L   V  S  A  G   D  R  V

ACCATAACCT GCAAGGCCAG TCAGAGTGTG AGTAATGATG TAGCTTGGTA    1250
 T  I  T   C  K  A  S   Q  S  V   S  N  D   V  A  W  Y

CCAACAGAAG CCAGGGCAGT CTCCTACACT GCTCATATCC TATACATCCA    1300
  Q  Q  K   P  G  Q   S  P  T  L   L  I  S   Y  T  S

GTCGCTACGC TGGAGTCCCT GATCGCTTCA TTGGCAGTGG ATATGGGACG    1350
S  R  Y  A   G  V  P   D  R  F   I  G  S  G   Y  G  T

GATTTCACTT TCACCATCAG CACTTTGCAG GCTGAAGACC TGGCAGTTTA    1400
 D  F  T   F  T  I  S   T  L  Q   A  E  D   L  A  V  Y

TTTCTGTCAG CAAGATTATA ATTCTCCTCC GACGTTCGGT GGAGGCACCA    1450
  F  C  Q   Q  D  Y   N  S  P  P   T  F  G   G  G  T

AGCTGGAAAT CAAATAA
K  L  E  I   K  .
```

FIG. 2 CONT'D

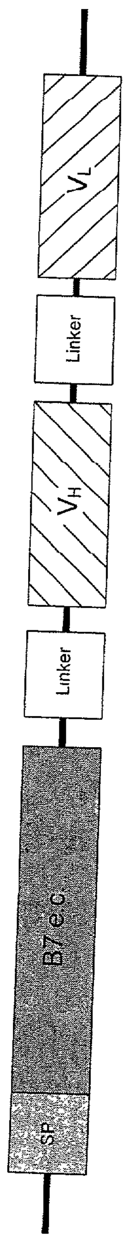

FIG. 3a

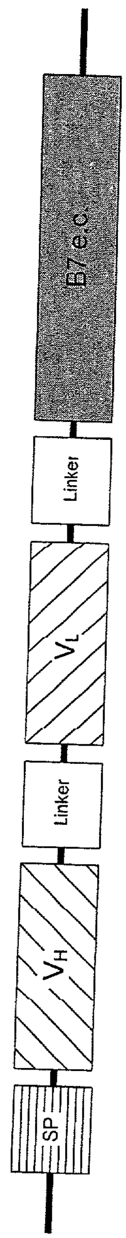

FIG. 3b

```
1    ATGGGACTGA GTAACATTCT CTTTGTGATG GCCTTCCTGC TCTCTGGTGC
      M  G  L   S  N  I  L   F  V  M   A  F  L   L  S  G  A

51   TGCTCCTCTG AAGATTCAAG CTTATTTCAA TGAGACTGCA GACCTGCCAT
       A  P  L   K  I  Q   A  Y  F  N   E  T  A   D  L  P

101  GCCAATTTGC AAACTCTCAA AACCAAAGCC TGAGTGAGCT AGTAGTATTT
      C  Q  F   A  N  S  Q   N  Q  S  L  S  E  L   V  V  F

151  TGGCAGGACC AGGAAAACTT GGTTCTGAAT GAGGTATACT TAGGCAAAGA
      W  Q  D   Q  E  N  L   V  L  N   E  V  Y   L  G  K  E

201  GAAATTTGAC AGTGTTCATT CCAAGTATAT GGGCCGCACA AGTTTTGATT
       K  F  D   S  V  H   S  K  Y  M   G  R  T   S  F  D

251  CGGACAGTTG GACCCTGAGA CTTCACAATC TTCAGATCAA GGACAAGGGC
     S  D  S  W   T  L  R   L  H  N   L  Q  I  K   D  K  G

301  TTGTATCAAT GTATCATCCA TCACAAAAAG CCCACAGGAA TGATTCGCAT
      L  Y  Q   C  I  I  H   H  K  K   P  T  G   M  I  R  I

351  CCACCAGATG AATTCTGAAC TGTCAGTGCT TGCTAACTTC AGTCAACCTG
       H  Q  M   N  S  E   L  S  V  L   A  N  F   S  Q  P

401  AAATAGTACC AATTTCTAAT ATAACAGAAA ATGTGTACAT AAATTTGACC
     E  I  V  P   I  S  N   I  T  E   N  V  Y  I   N  L  T

451  TGCTCATCTA TACACGGTTA CCCAGAACCT AAGAAGATGA GTGTTTTGCT
      C  S  S   I  H  G  Y   P  E  P   K  K  M   S  V  L  L

501  AAGAACCAAG AATTCAACTA TCGAGTATGA TGGTATTATG CAGAAATCTC
       R  T  K   N  S  T   I  E  Y  D   G  I  M   Q  K  S

551  AAGATAATGT CACAGAACTG TACGACGTTT CCATCAGCTT GTCTGTTTCA
     Q  D  N  V   T  E  L   Y  D  V   S  I  S  L   S  V  S

601  TTCCCTGATG TTACGAGCAA TATGACCATC TTCTGTATTC TGGAAACTGA
      F  P  D   V  T  S  N   M  T  I   F  C  I   L  E  T  D

651  CAAGACGCGG CTTTTATCTT CACCTTTCTC TATAGAGCTT GAGGACCCTC
       K  T  R   L  L  S   S  P  F  S   I  E  L   E  D  P

701  AGCCTCCCCC AGACCACATT CCTGGAGGCG GGGGATCC
     Q  P  P  P   D  H  I   P  G  G   G  G  S
```

FIG. 4

FIG. 5

```
atggcttgca attgtcagtt gatgcaggat acaccactcc tcaagtttcc atgtccaagg 60
ctcattcttc tctttgtgct gctgattcgt ctttcacaag tgtcttcaga tgttgatgaa 120
caactgtcca agtcagtgaa agataaggta ttgctgcctt gccgttacaa ctctccgcat 180
gaagatgagt ctgaagaccg aatctactgg caaaaacatg acaaagtggt gctgtctgtc 240
attgctggga aactaaaagt gtggcccgag tataagaacc ggactttata tgacaacact 300
acctactctc ttatcatcct gggcctggtc ctttcagacc ggggcacata cagctgtgtc 360
gttcaaaaga aggaaagagg aacgtatgaa gttaaacact tggctttagt aaagttgtcc 420
atcaaagctg acttctctac ccccaacata actgagtctg gaaacccatc tgcagacact 480
aaaaggatta cctgctttgc ttccgggggt ttcccaaagc ctcgcttctc ttggttggaa 540
aatggaagag aattacctgg catcaatacg acaatttccc aggatcctga atctgaattg 600
tacaccatta gtagccaact agatttcaat acgactcgca accacaccat taagtgtctc 660
attaaatatg gagatgctca cgtgtcagag gacttcacct gggaaaaacc cccagaagac 720
cctcctgata gcaagcccgg gggtggtggg agcggtggtg gcggcagtgg cggcggcgga 780
actagtgagg tccagcttca gcagtctgga cctgacctgg tgaagcctgg ggcttcagtg 840
aagatatcct gcaaggcttc tggttactca ttcactggct actacatgca ctgggtgaag 900
cagagccatg gaaagagcct tgagtggatt ggacgtatta atcctaacaa tggtgttact 960
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tctactatga ttacgaacta tgttatggac tactggggtc aagtaacttc agtcaccgtc 1140
tcttcaggtg gtggtgggag cggtggtggc ggcactggcg gcggcggatc tagtattgtg 1200
atgacccaga ctcccacatt cctgcttgtt tcagcaggag acagggttac cataacctgc 1260
aaggccagtc agagtgtgag taatgatgta gcttggtacc aacagaagcc agggcagtct 1320
cctacactgc tcatatccta tacatccagt cgctacgctg gagtccctga tcgcttcatt 1380
ggcagtggat atgggacgga tttcactttc accatcagca ctttgcaggc tgaagacctg 1440
gcagtttatt tctgtcagca agattataat tctcctccga cgttcggtgg aggcaccaag 1500
ctggaaatca aacggtaa                                             1518
```

FIG. 6

Leader / 5T4 scFv / HIgG DNA and deduced protein sequence

```
CTCGAGCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCGAGGTCCAGCTG
            M  G  W  S  C  I  I  L  F  L  V  A  T  A  T  G  V  H  S  E  V  Q  L

CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGG
 Q  Q  S  G  P  D  L  V  K  P  G  A  S  V  K  I  S  C  K  A  S  G  Y  S  F  T

CTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTA
G  Y  Y  M  H  W  V  K  Q  S  H  G  K  S  L  E  W  I  G  R  I  N  P  N  N  G  V

CTCTCTACAACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC
 T  L  Y  N  Q  K  F  K  D  K  A  I  L  T  V  D  K  S  S  T  T  A  Y  M  E  L  R

AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAACTATGTTATGGACTACTGGGG
 S  L  T  S  E  D  S  A  V  Y  Y  C  A  R  S  T  M  I  T  N  Y  V  M  D  Y  W

TCAAGTAACTTCAGTCACCGTCTCTTCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTG
G  Q  V  T  S  V  T  V  S  S  G  G  G  G  S  G  G  G  G  T  G  G  G  G  S  S  I

TGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG
 V  M  T  Q  T  P  T  F  L  L  V  S  A  G  D  R  V  T  I  T  C  K  A  S  Q  S  V

AGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGC
 S  N  D  V  A  W  Y  Q  Q  K  P  G  Q  S  P  T  L  L  I  S  Y  T  S  S  R  Y

TCCAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACC
A  G  V  P  D  R  F  I  G  S  G  Y  G  T  D  F  T  F  T  I  S  T  L  Q  A  E  D

TGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAAATCAAACGGGCC
 L  A  V  Y  F  C  Q  Q  D  Y  N  S  P  P  T  F  G  G  G  T  K  L  E  I  K  R  A

TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT
 S  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C

GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGG
L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P

CTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
 A  V  L  Q  S  S  G  L  Y  S  L  S  S  V  V  T  V  P  S  S  S  L  G  T  Q  T  Y

ATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACAC
 I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K  V  E  P  K  S  C  D  K  T  H

ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA
T  C  P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D  T  L

TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGT
 V  D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S

CCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P  A  P

TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  M

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG
 T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N

GCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCG
G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T

TGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
 V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q

AAGAGCCTCTCCCTGTCCCCGGGTAAATGACTCGAG
 K  S  L  S  L  S  P  G  K  .
```

FIG. 7

```
ctcgagccac catgggatgg agctgtatca tcctcttctt ggtagcaaca gctacaggtg 60
tccactccga ggtccagctg cagcagtctg gacctgacct ggtgaagcct ggggcttcag 120
tgaagatatc ctgcaaggct tctggttact cattcactgg ctactacatg cactgggtga 180
agcagagcca tggaaagagc cttgagtgga ttggacgtat taatcctaac aatggtgtta 240
ctctctacaa ccagaaattc aaggacaagg ccatattaac tgtagacaag tcatccacca 300
cagcctacat ggagctccgc agcctgacat ctgaggactc tgcggtctat tactgtgcaa 360
gatctactat gattacgaac tatgttatgg actactgggg tcaagtaact tcagtcaccg 420
tctcttcagg tggtggtggg agcggtggtg gcggcactgg cggcggcgga tctagtattg 480
tgatgaccca gactcccaca ttcctgcttg tttcagcagg agacagggtt accataacct 540
gcaaggccag tcagagtgtg agtaatgatg tagcttggta ccaacagaag ccagggcagt 600
ctcctacact gctcatatcc tatacatcca gtcgctacgc tggagtccct gatcgcttca 660
ttggcagtgg atatgggacg gatttcactt tcaccatcag cactttgcag gctgaagacc 720
tggcagttta tttctgtcag caagattata attctcctcc gacgttcggt ggaggcacca 780
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atggcacgtt aaccgtcacg tccaccctgc cggtgggcac ccgagactgg atcgaggggg 1680
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ccaagaccag cggcccgcgt gctgccccgg aagtctatgc gtttgcgacg ccggagtggc 1800
cggggagccg ggacaagcgc accctcgcct gcctgatcca gaacttcatg cctgaggaca 1860
tctcggtgca gtggctgcac aacgaggtgc agctcccgga cgcccggcac agcacgacgc 1920
agccccgcaa gaccaagggc tccggcttct tcgtcttcag ccgcctggag gtgaccaggg 1980
ccgaatggga gcagaaagat gagttcatct gccgtgcagt ccatgaggca gcgagcccct 2040
cacagaccgt ccagcgagcg gtgtctgtaa atcccggtaa atgagagctc            2090
```

FIG. 8

```
atggcttgca attgtcagtt gatgcaggat acaccactcc tcaagtttcc atgtccaagg 60
ctcattcttc tctttgtgct gctgattcgt ctttcacaag tgtcttcaga tgttgatgaa 120
caactgtcca agtcagtgaa agataaggta ttgctgcctt gccgttacaa ctctccgcat 180
gaagatgagt ctgaagaccg aatctactgg caaaaacatg acaaagtggt gctgtctgtc 240
attgctggga aactaaaagt gtggcccgag tataagaacc ggactttata tgacaacact 300
acctactctc ttatcatcct gggcctggtc ctttcagacc ggggcacata cagctgtgtc 360
gctcaaaaga aggaaagagg aacgtatgaa gttaaacact tggctttagt aaagttgtcc 420
atcaaagctg acttctctac ccccaacata actgagtctg gaaacccatc tgcagacact 480
aaaaggatta cctgctttgc ttccgggggt ttcccaaagc ctcgcttctc ttggttggaa 540
aatggaagag aattacctgg catcaatacg acaatttccc aggatcctga atctgaattg 600
tacaccatta gtagccaact agatttcaat acgactcgca accacaccat taagtgtctc 660
attaaatatg gagatgctca cgtgtcagag gacttcacct gggaaaaacc cccagaagac 720
cctcctgata gcaagcccgg gggtggtggg agcggtggtg gcggcagtgg cggcggcgga 780
actagtaata gtgactctga atgtcccctg tcccacgatg ggtactgcct ccatgatggt 840
gtgtgcatgt atattgaagc attggacaag tatgcatgca actgtgttgt tggctacatc 900
ggggagcgat gtcagtaccg agacctgaag tggtgggaac tgcgc                 945
```

FIG. 9

CT26-neo Transfectants

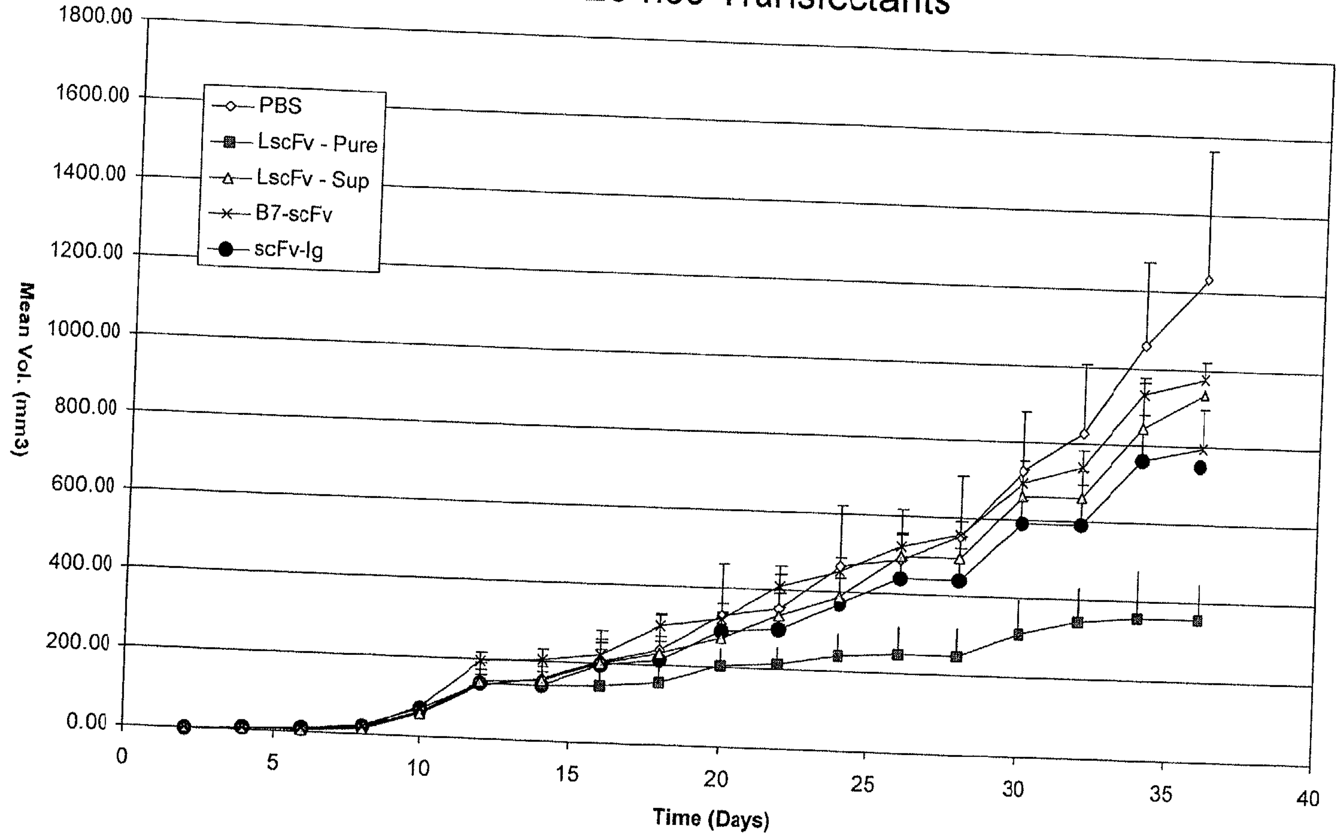


FIG. 10

CT26-h5T4 Transfectants

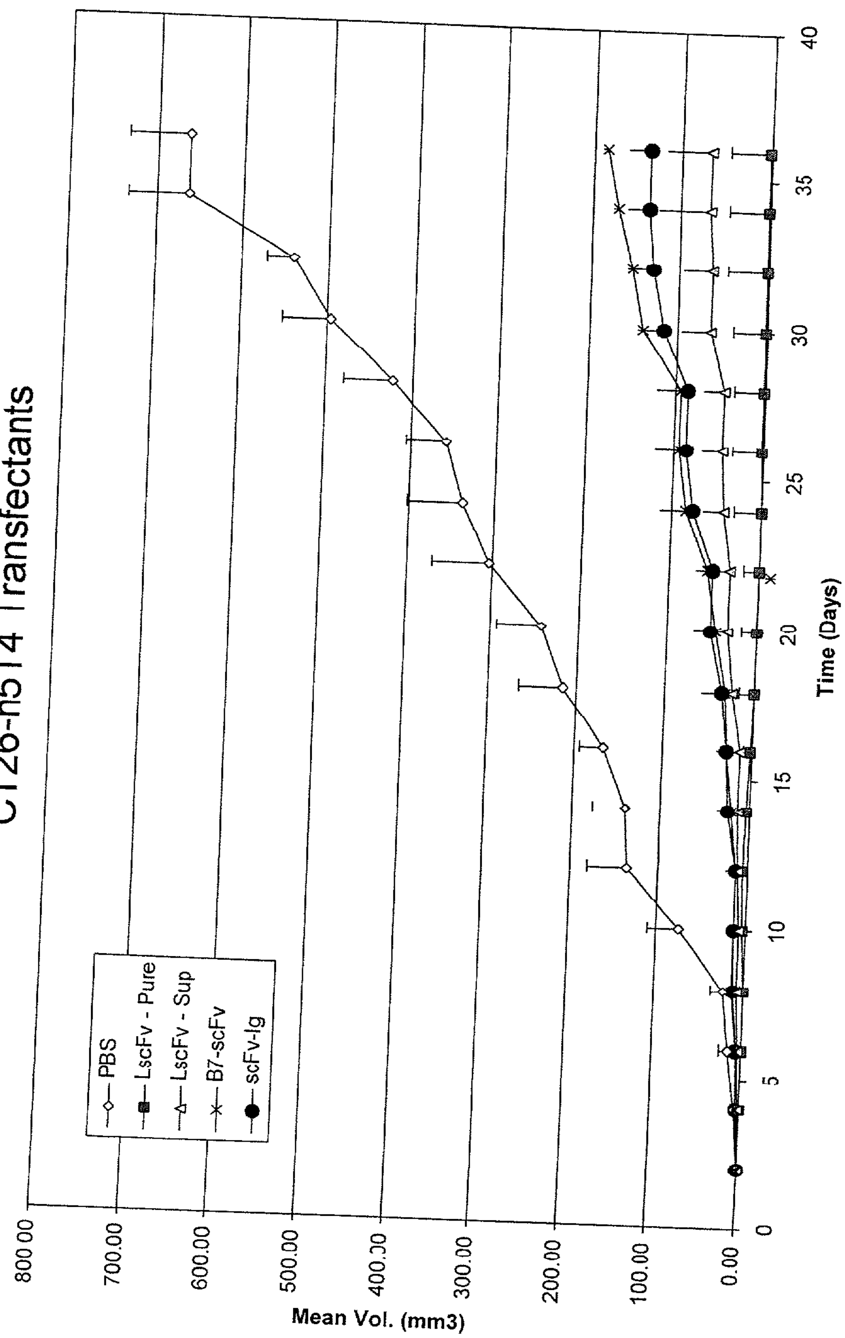


FIG. 11

B16-h5T4 Tumour Growth

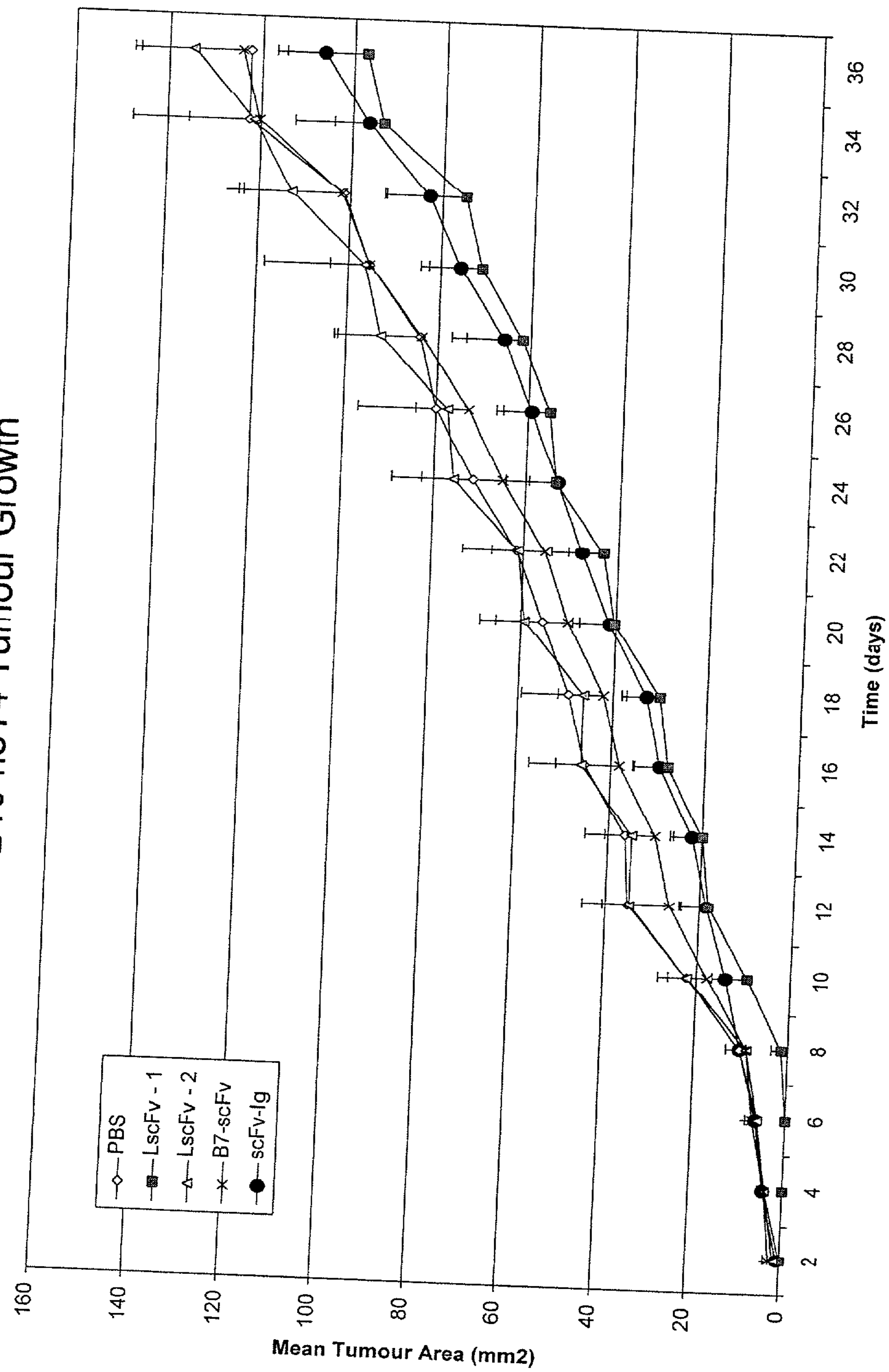
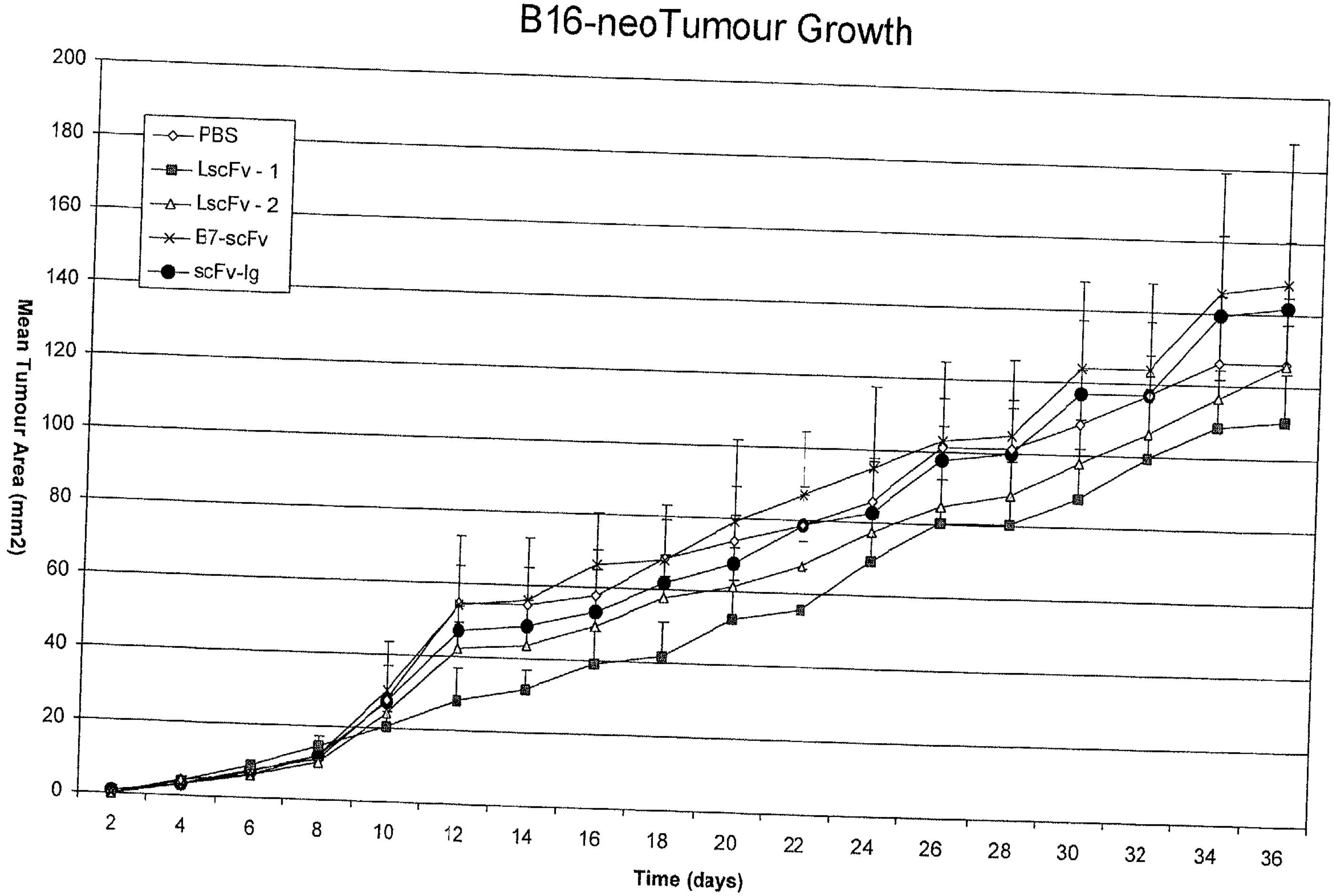


FIG. 12


B16-neoTumour Growth
PBS
LscFv - 1
LscFv - 2
B7-scFv
scFv-Ig
Mean Tumour Area (mm2)
200
180
160
140
120
100
80
60
40
20
0
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
32
34
36
Time (days)

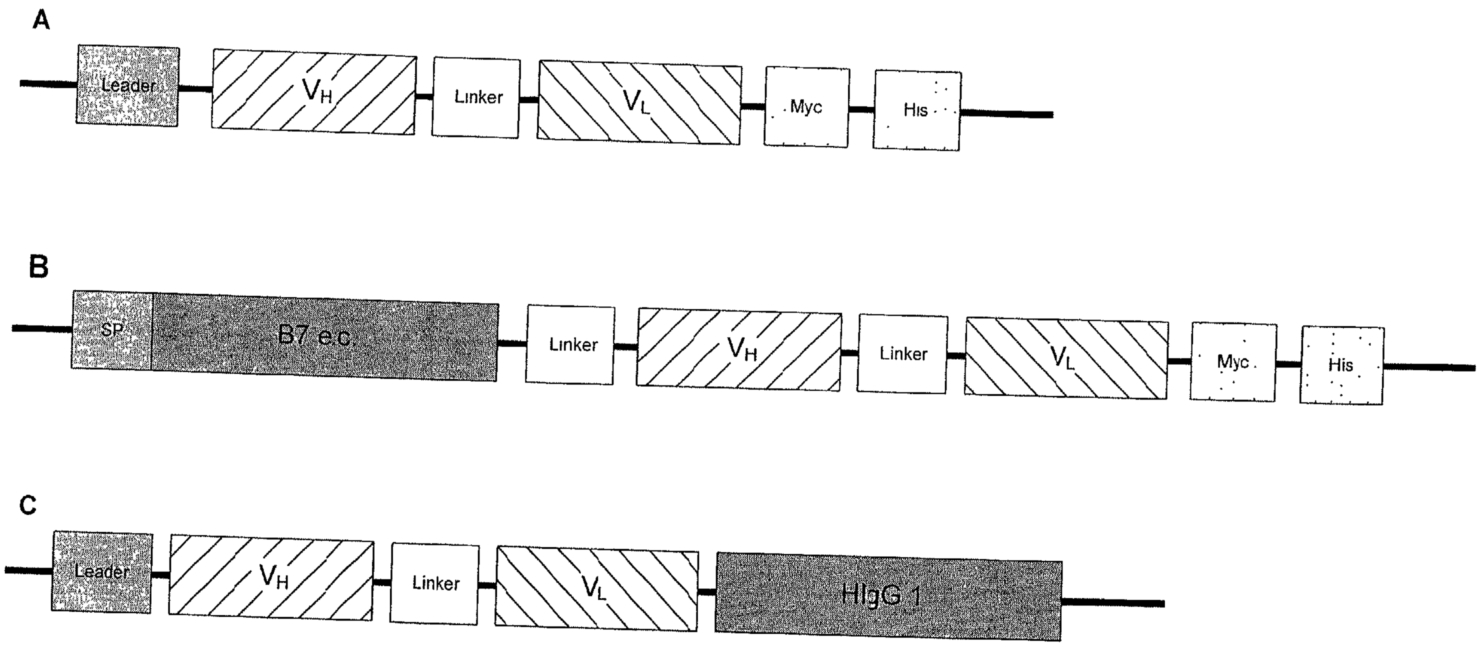

A
Leader
V_H
Linker
V_L
Myc
His
B
SP
B7 e.c.
Linker
V_H
Linker
V_L
Myc
His
C
Leader
V_H
Linker
V_L
HIgG 1

FIG. 13

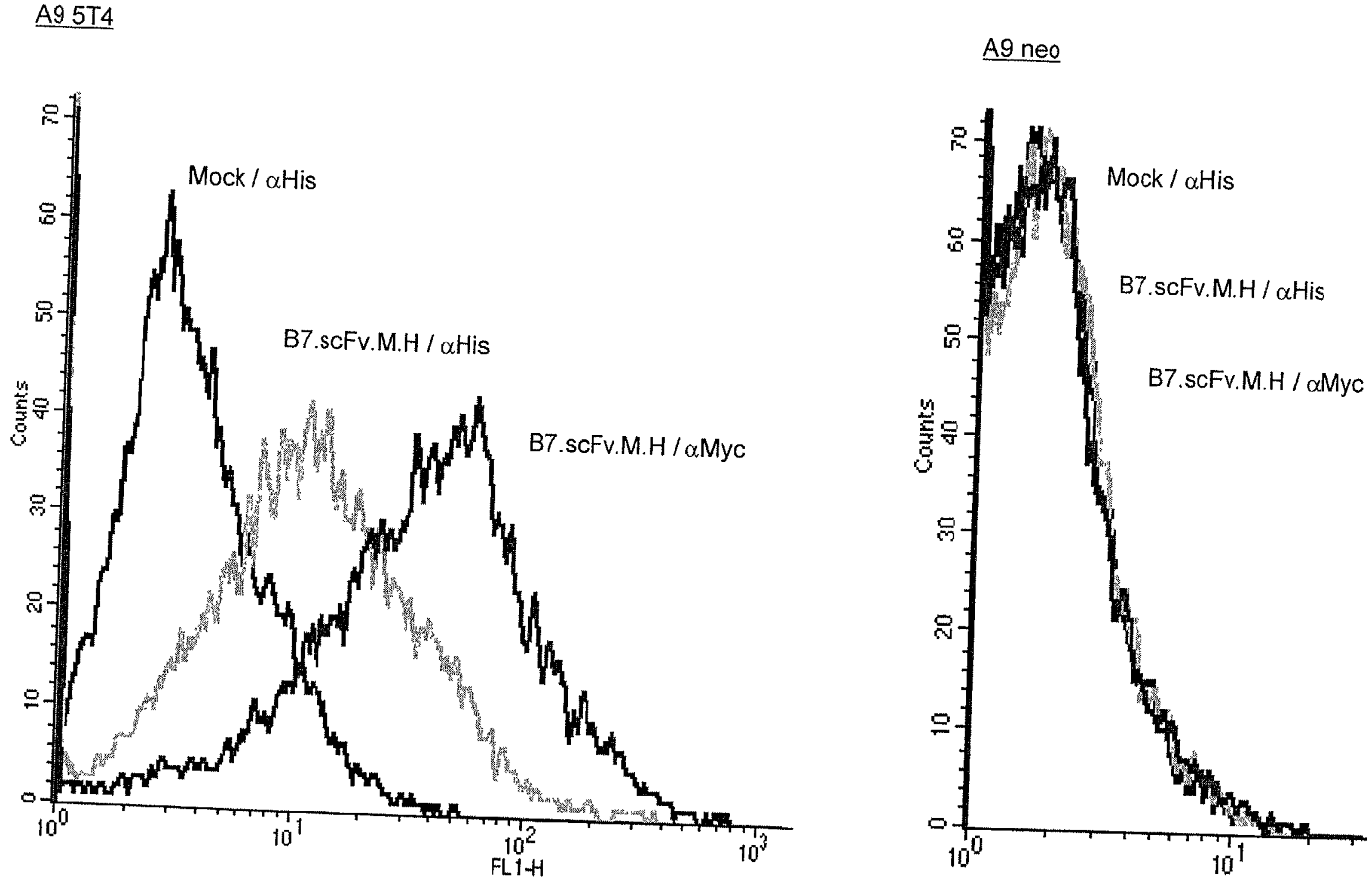
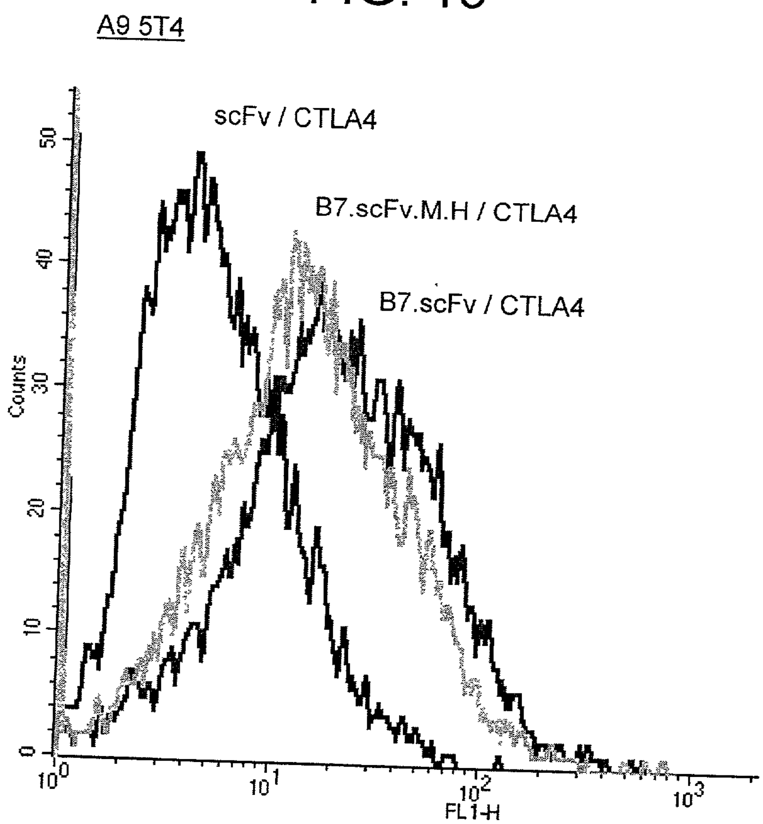

A9 5T4
Mock / αHis
B7.scFv.M.H / αHis
B7.scFv.M.H / αMyc
Counts
0
10
20
30
40
50
60
70
10^0
10^1
10^2
10^3
FL1-H
A9 neo
Mock / αHis
B7.scFv.M.H / αHis
B7.scFv.M.H / αMyc
Counts
0
10
20
30
40
50
60
70
10^0
10^1

FIG. 14

FIG. 15


A9 5T4
scFv / CTLA4
B7.scFv.M.H / CTLA4
B7.scFv / CTLA4
Counts
0
10
20
30
40
50
10^0
10^1
10^2
10^3
FL1-H

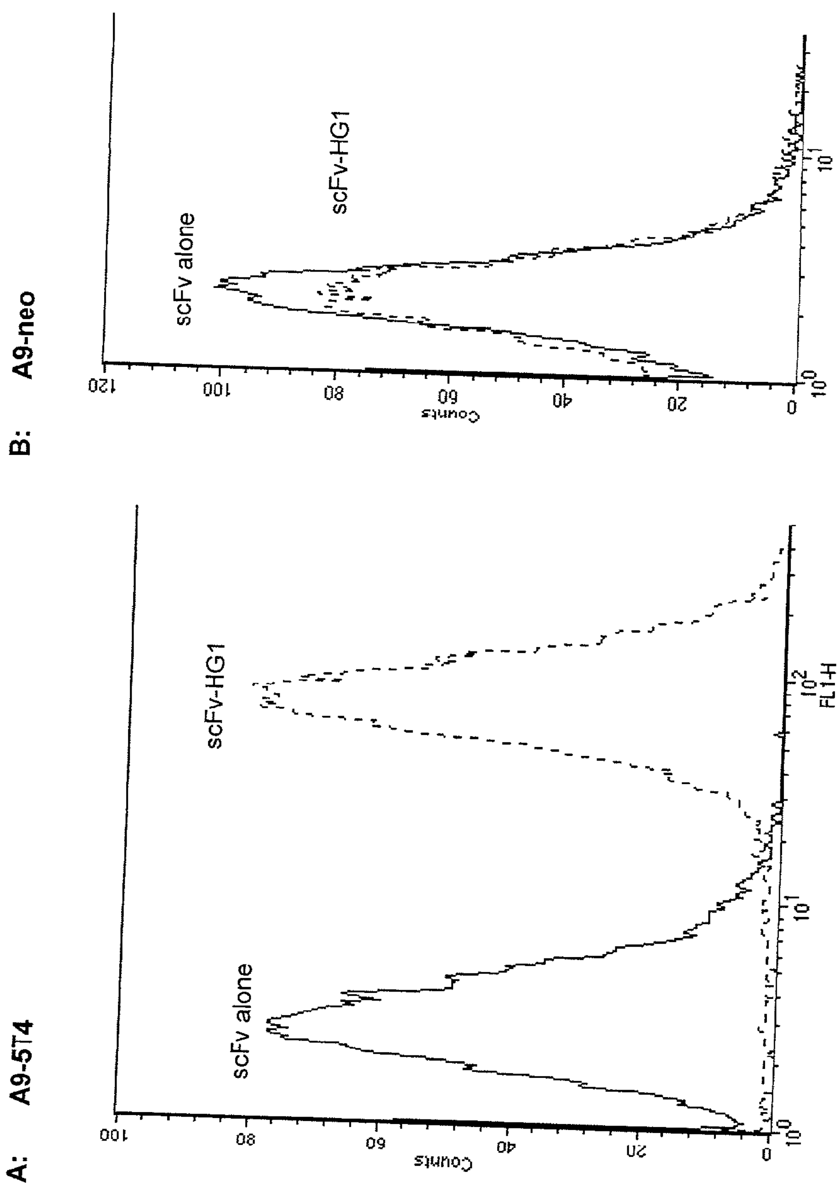
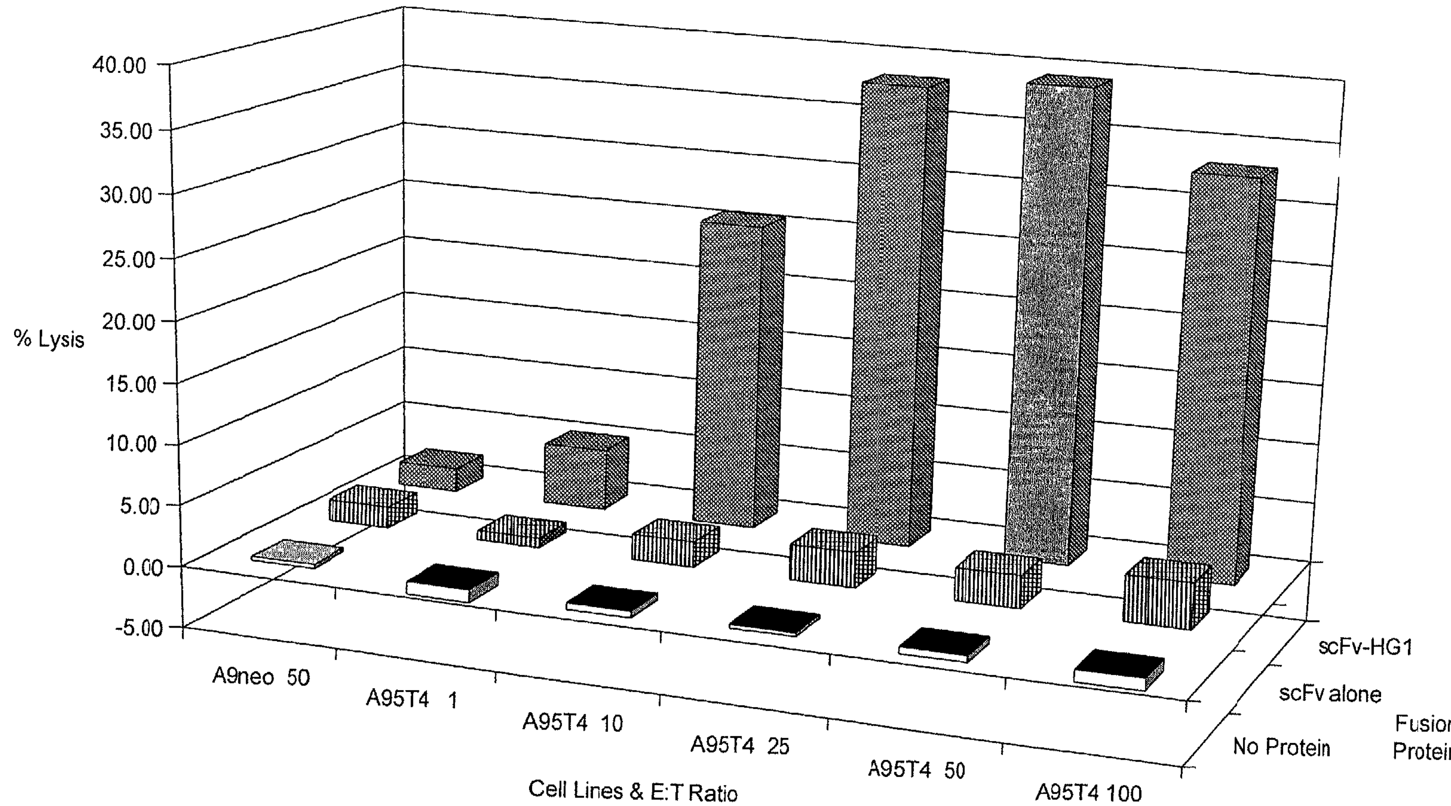

A:
A9-5T4
scFv alone
scFv-HG1
Counts
FL1-H
B:
A9-neo
scFv alone
scFv-HG1
Counts

FIG. 16

FIG. 17



% Lysis
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
-5.00
A9neo 50
A95T4 1
A95T4 10
A95T4 25
A95T4 50
A95T4 100
Cell Lines & E:T Ratio
scFv-HG1
scFv alone
No Protein
Fusion Protein

FIG. 18

pONY8.1SM

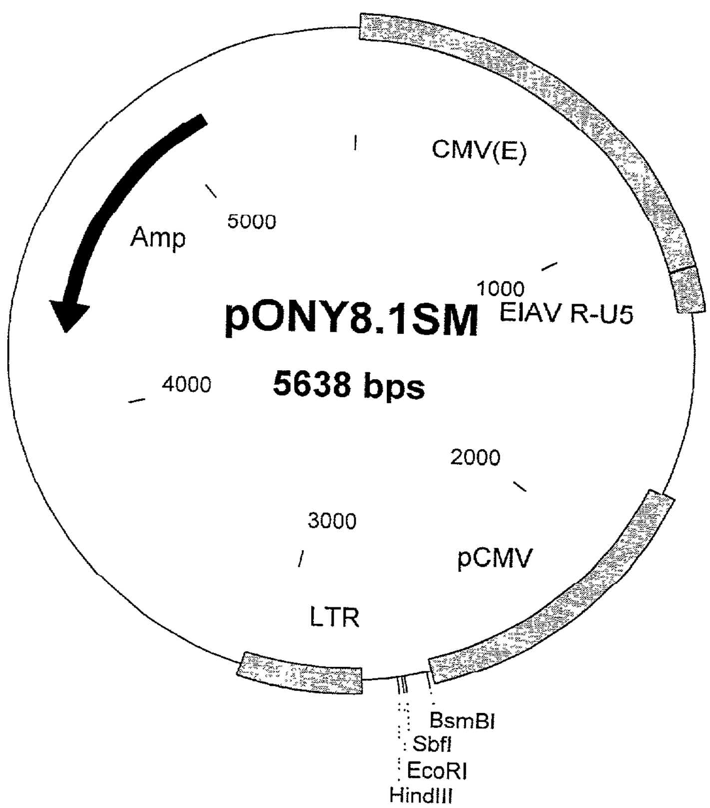
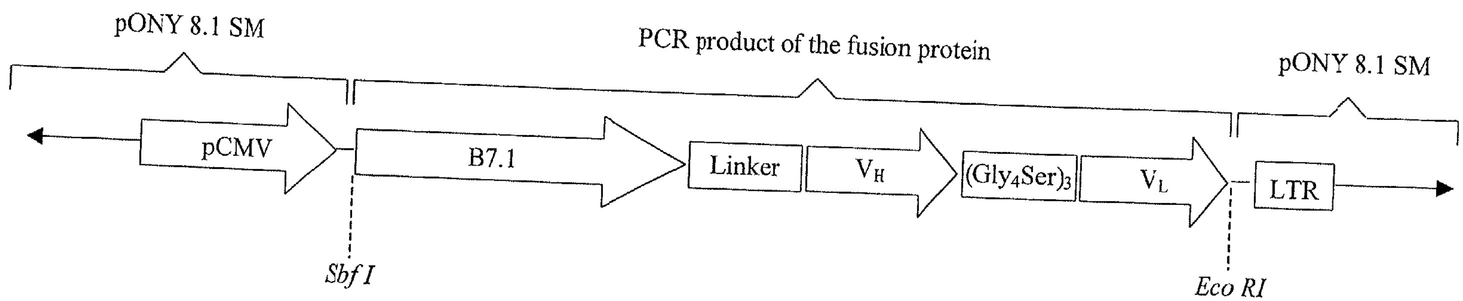


FIG. 19

FUSION PROTEIN CONSTRUCTS IN pONY 8.1SM

A. B7-5T4scFv



B. L-5T4scFv

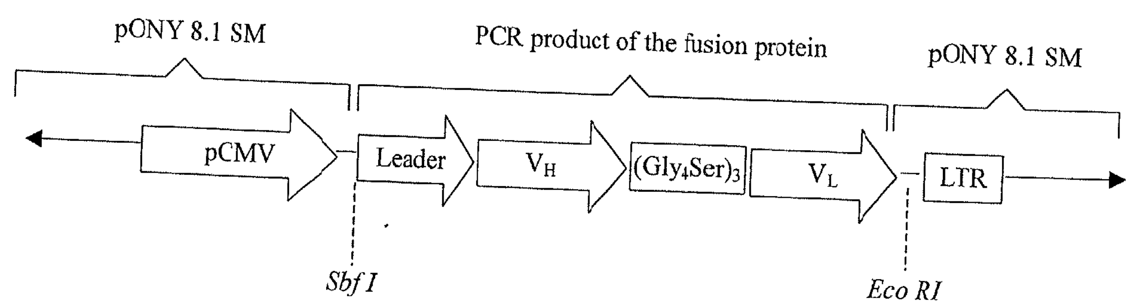


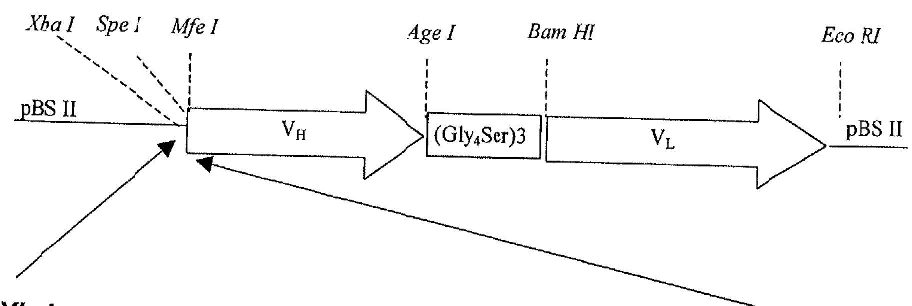
FIG. 20

pKLink – the $(Gly_4Ser)_3$ linker in pBluescript II SK (pBS II)

```
                            Age I
                     Spe I
NotI    XbaI        CTAGTACCGGTGGTGGTGGGAGCGGTGGTGGCGGCAGTGGCGGCGGCG    Bam HI
   pBS II               ATGGCCACCACCACCCTCGCCACCACCGCCGTCACCGCCGCCGCCTAG     SmaI ——▶ SalI
                           G  G  G  G  S  G  G  G  G  S  G  G  G  G  S         pBS II
```

FIG. 21

An scFv and leader sequence in pBSII



XbaI

```
CTAGACCTGCAGGCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCC
    TGGACGTCCGGTGGTACCCTACCTCGACATAGTAGGAGAAGAACCATCGTTGTCGATGTCCACATGTGAGGGTTAA
     Sbf I                                                                    Mfe I
```

FIG. 22

Leader-IL-5 scFv in pONY 8.1SM

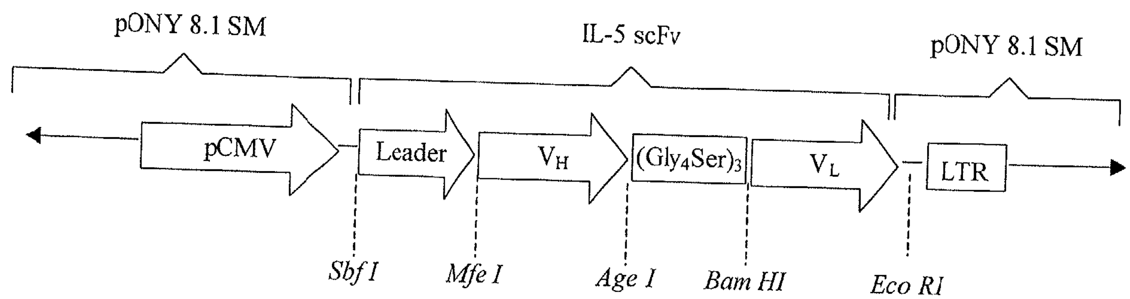


FIG. 23

Leader-HIV gp120 scFv in pONY 8.1SM

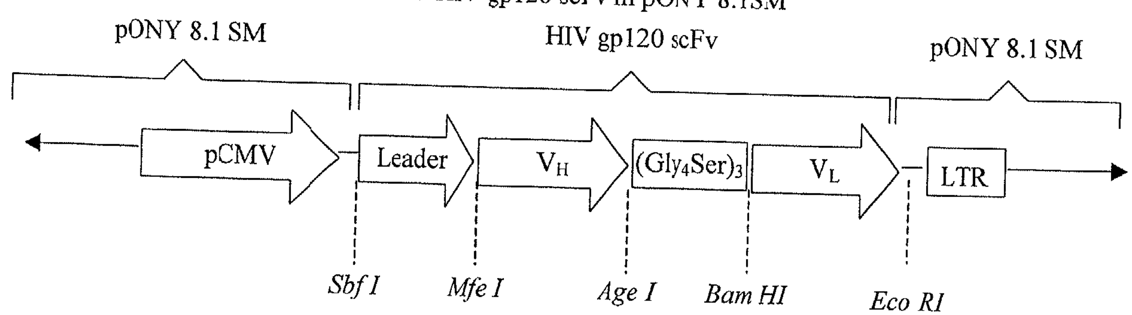


FIG. 24

pAdApt

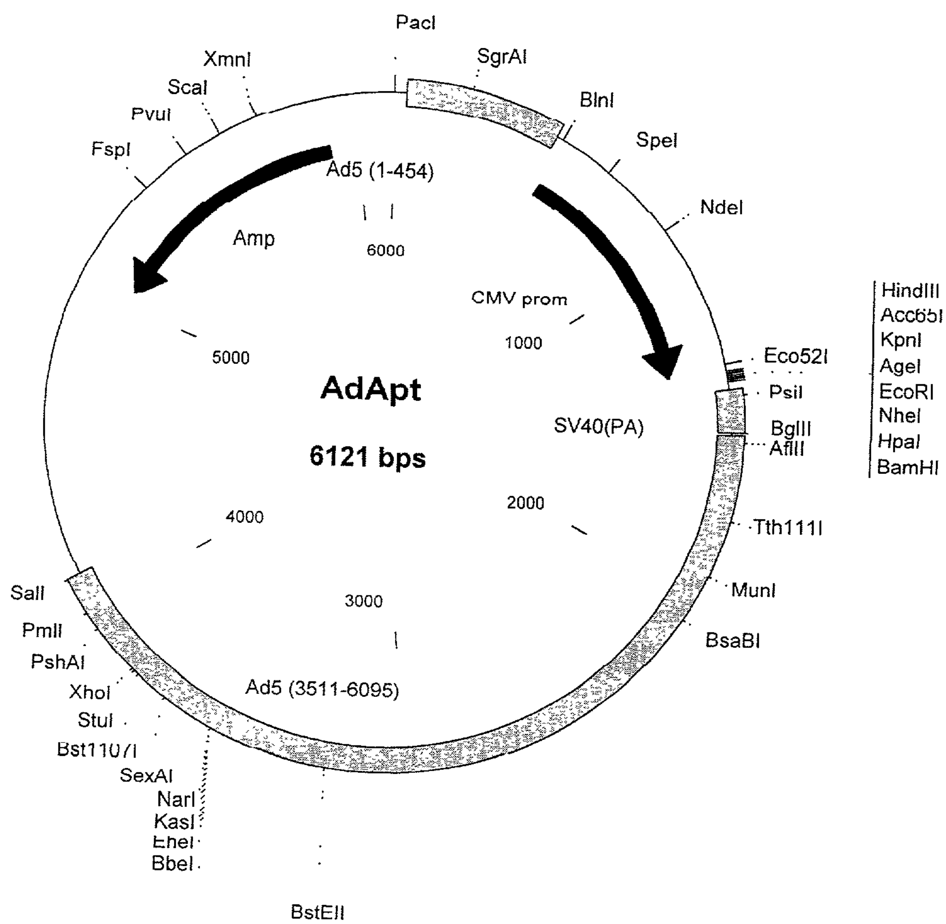
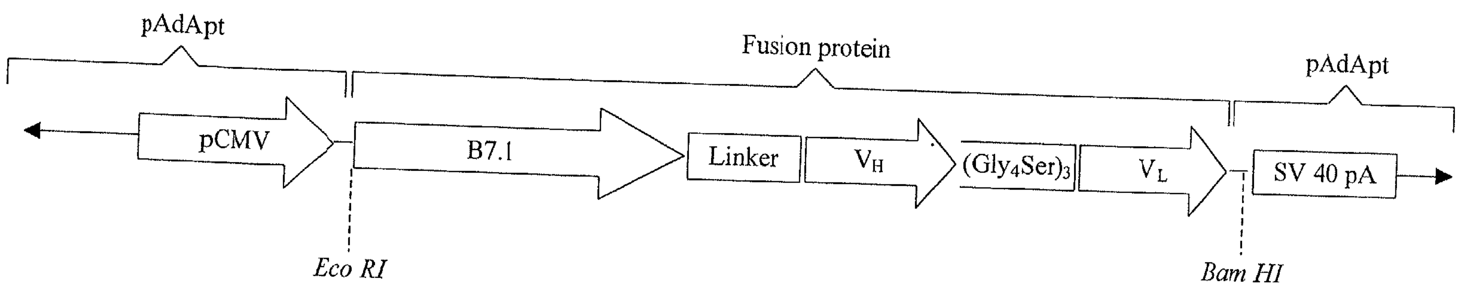


FIG. 25

FUSION PROTEIN CONSTRUCTS IN pAdApt

A. B7-5T4scFv



B. L-5T4scFv

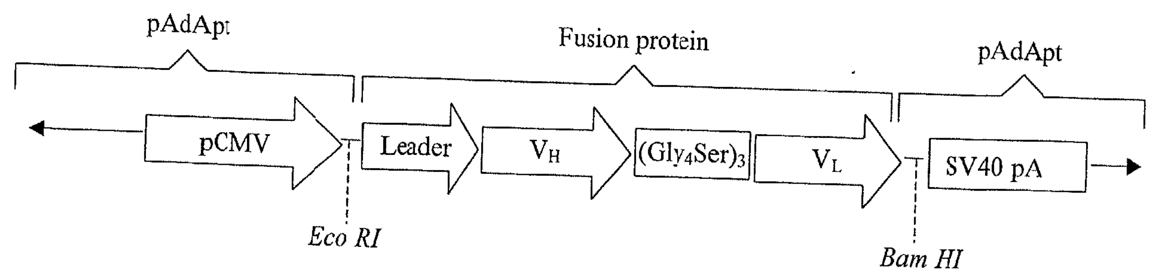


FIG. 26

Canine 5T4 Coding Sequence

```
ATGCCTGGGGGGTGCTCCCGGGGCCCCGCCGCCGGGGACGGGCGGTTGCGGCTGGCGCGGCTGGCGCTGGTGCTCCTGGG 80
  M  P  G  G  C  S  R  G  P  A  A  G  D  G  R  L  R  L  A  R  L  A  L  V  L  L

CTGGGTCTCCTCGTCCTCGCTCACCTCCTGGGCGCCCTCCGCCGCCGCCTCCACGTCGCCGCCGGCCTCCGCGGCGTCCG 160
G  W  V  S  S  S  S  L  T  S  W  A  P  S  A  A  A  S  T  S  P  P  A  S  A  A  S

CCCCGCCCCCGCTGCCGGGCCAGTGCCCCCAGCCTTGCGAGTGCTCGGAGGCGGCGCGCACGGTCAAGTGCGTTAACCGC 240
 A  P  P  P  L  P  G  Q  C  P  Q  P  C  E  C  S  E  A  A  R  T  V  K  C  V  N  R

AACCTGACCGAGGTGCCCGCGGACCTGCCCCCCTACGTGCGCAACCTCTTCCTCACGGGCAACCAGCTGGCGGTGCTGCC 320
  N  L  T  E  V  P  A  D  L  P  P  Y  V  R  N  L  F  L  T  G  N  Q  L  A  V  L

CCCCGGCGCCTTCGCCCGCCGGCCGCCGCTGGCCGAGCTGGCCGCGCTCAACCTGAGCGGCAGCAGCCTGCGGGAGGTGT 400
P  P  G  A  F  A  R  R  P  P  L  A  E  L  A  A  L  N  L  S  G  S  S  L  R  E  V

GCGCCGGCGCCTTCGAGCACCTGCCCAGCCTGCGCCAGCTCGACCTCAGCCACAACCCGCTGGGCAACCTCAGCGCCTTC 480
 C  A  G  A  F  E  H  L  P  S  L  R  Q  L  D  L  S  H  N  P  L  G  N  L  S  A  F

GCCTTCGCGGGCAGCGACGCCAGCCGCTCGGGCCCCAGCCCCCTGGTGGAGCTGATGCTGAACCACATCGTGCCCCCCGA 560
  A  F  A  G  S  D  A  S  R  S  G  P  S  P  L  V  E  L  M  L  N  H  I  V  P  P

CGACCGGCGGCAGAACCGGAGCTTCGAGGGCATGGTGGCGGCTGCCCTCCGAGCGGGCCGCGCGCTTCGCGGGCTGCAGT 640
D  D  R  R  Q  N  R  S  F  E  G  M  V  A  A  A  L  R  A  G  R  A  L  R  G  L  Q

GCCTGGAGCTGGCCGGCAACCGCTTCCTCTACTTGCCTCGCGACGTCCTGGCCCAGCTACCCGGCCTCCGGCACCTGGAC 720
 C  L  E  L  A  G  N  R  F  L  Y  L  P  R  D  V  L  A  Q  L  P  G  L  R  H  L  D

CTGCGCAACAACTCCCTGGTGAGCCTCACCTACGTGTCCTTCCGCAACCTGACGCACTTGGAGAGCCTCCACCTGGAGGA 800
  L  R  N  N  S  L  V  S  L  T  Y  V  S  F  R  N  L  T  H  L  E  S  L  H  L  E

CAACGCCCTCAAGGTCCTTCACAACGCCACCCTGGCGGAGCTGCAGAGCCTGCCCCACGTCCGGGTCTTCCTGGACAACA 880
D  N  A  L  K  V  L  H  N  A  T  L  A  E  L  Q  S  L  P  H  V  R  V  F  L  D  N

ACCCCTGGGTCTGCGATTGTCACATGGCAGACATGGTGGCCTGGCTCAAGGAGACAGAGGTGGTGCCGGGCAAAGCCGGG 960
 N  P  W  V  C  D  C  H  M  A  D  M  V  A  W  L  K  E  T  E  V  V  P  G  K  A  G

CTCACCTGTGCATTCCCGGAGAAAATGAGGAATCGGGCCCTCTTGGAACTCAACAGCTCCCACCTGGACTGTGACCCTAT 1040
  L  T  C  A  F  P  E  K  M  R  N  R  A  L  L  E  L  N  S  S  H  L  D  C  D  P

CCTCCCTCCATCCCTGCAGACTTCTTATGTCTTCCTAGGTATTGTCTTAGCCCTGATAGGCGCCATCTTCCTACTGGTTT 1120
I  L  P  P  S  L  Q  T  S  Y  V  F  L  G  I  V  L  A  L  I  G  A  I  F  L  L  V

TGTATTTGAACCGCAAGGGGATAAAGAAGTGGATGCATAACATCAGAGATGCCTGCAGGGATCACATGGAAGGGTATCAC 1200
 L  Y  L  N  R  K  G  I  K  K  W  M  H  N  I  R  D  A  C  R  D  H  M  E  G  Y  H

TACAGATACGAAATCAATGCAGACCCCAGGTTAACAAACCTCAGTTCCAATTCGGATGTCTGA                  1263
  Y  R  Y  E  I  N  A  D  P  R  L  T  N  L  S  S  N  S  D  V  .
```